

P0102402

Title: ANTIBODY RECOGNIZING GM1
GANGLIOSIDE-BOUND ...
By: Katsuhiko YANAGISAWA, et al.
Docket No.: 040036

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Fig. 1

Filename : A β antibody heavy chain variable region
Sequence Size : 408
Sequence Position: 1 - 408

signal sequence

10	20	30	40	50	60
M	G	W	I	W	I
G	W	I	W	I	F
ATGGGATGGATCTGGATCTTCTCTCCCTGTCAGGAAC	TGCAGGTGTCCACTCTGAG				

70	80	90	100	110	120
V	Q	L	Q	S	G
G	T	C	Q	S	P
TGCCAGCTGCAGCAGTCTGGACCTGAGCTAGTGAAGA	CTGGGGCTTCAGTGAAGATA	TCC	CAT	TCC	ATCC

CDR1

130	140	150	160	170	180
TGCAAGGCTTCTGGTTACTCATTCACTGGTTACTACAT	GCAC	GGTCAAGCAGAGCCAT			
C	K	A	S	G	Y
K	A	S	G	Y	S
A	S	G	Y	S	F
S	F	T	G	Y	Y
T	G	H	M	H	W

CDR2

190	200	210	220	230	240
GGAAAGAGCCTTGAGTGGATTGGATATATTAGTTGTTACA	ATGGTGTACTAGCTACAAC				
G	K	S	L	E	W
K	S	L	E	W	I
S	L	E	W	I	G
L	E	W	I	G	Y
E	W	I	G	Y	I
W	I	G	Y	I	S
I	G	Y	I	S	C
G	Y	I	S	C	Y
Y	I	S	C	Y	N
I	S	C	Y	N	G
S	C	Y	N	G	A
C	Y	N	G	A	T
Y	N	G	A	T	S
N	G	A	T	S	Y
G	A	T	S	Y	N

CDR3

310	320	330	340	350	360
CAGTTCAACAGCCTGACATCTGAAGACTCTGCGGTCTATT	ACTGTGCAAGAGGGGCTAAC				
Q	F	N	S	L	T
F	N	S	L	T	S
N	S	L	T	S	E
S	L	T	S	E	D
L	T	S	E	D	S
T	S	E	D	S	A
S	E	D	S	A	V
E	D	S	A	V	Y
D	S	A	V	Y	Y
S	A	V	Y	Y	C
A	V	Y	Y	C	A
V	Y	Y	C	A	R
Y	Y	C	A	R	G
Y	Y	A	R	G	A
Y	Y	R	G	A	N

370	380	390	400		
TGGGTCTTGACTACTGGGGCCAAGGCACC	ACTCTCACAGTCTCCTCA				
W	V	F	D	Y	W
V	F	D	Y	W	G
F	D	Y	W	G	Q
D	Y	W	G	Q	G
Y	W	G	G	G	T
W	G	G	T	T	L
G	G	T	T	L	T
G	T	T	L	T	V
T	L	L	T	V	S
L	T	L	T	S	S

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F i g . 2

Filename : A β antibody light chain variable region
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Sequence Position: 1 - 387

signal sequence

10 20 30 40 50 60
ATGGCCTGGACTTCACTTAACTCTCTCTCTGGCTCTGCTCAGGAGCCAGTTCCAG
M A W T S L I L S L L A L C S G A S S Q

70 80 90 100 110 120
GCTGTTGTGACTCAGGAATCTGCACTCACCACATCACCTGGTGGAACAGTCATACTCACT
A V V T Q E S A L T T S P G G T V I L T

CDR1

130 140 150 160 170 180
TGTCGCTCAAGTACTGGGCTGTTACAACACTAGTAACATGCCAAGGGTCCAAGAAAAAA
C R S S T G A V T T S N Y A N W V Q E K

CDR2

190 200 210 220 230 240
CCAGATCATTTATTCACTGGTCTAATAGGTGGTACCGAGCAACCGAGCTCCAGGTGTTCCCT
P D H L F T G L I G G T S N R A P G V P

250 260 270 280 290 300
GTCAGATTCTCAGGCTCCCTGATGGAGACAAGGCTGCCCTCACCATCACAGGGCACAG
V R F S G S L I G D K A A L T I T G A Q

CDR3

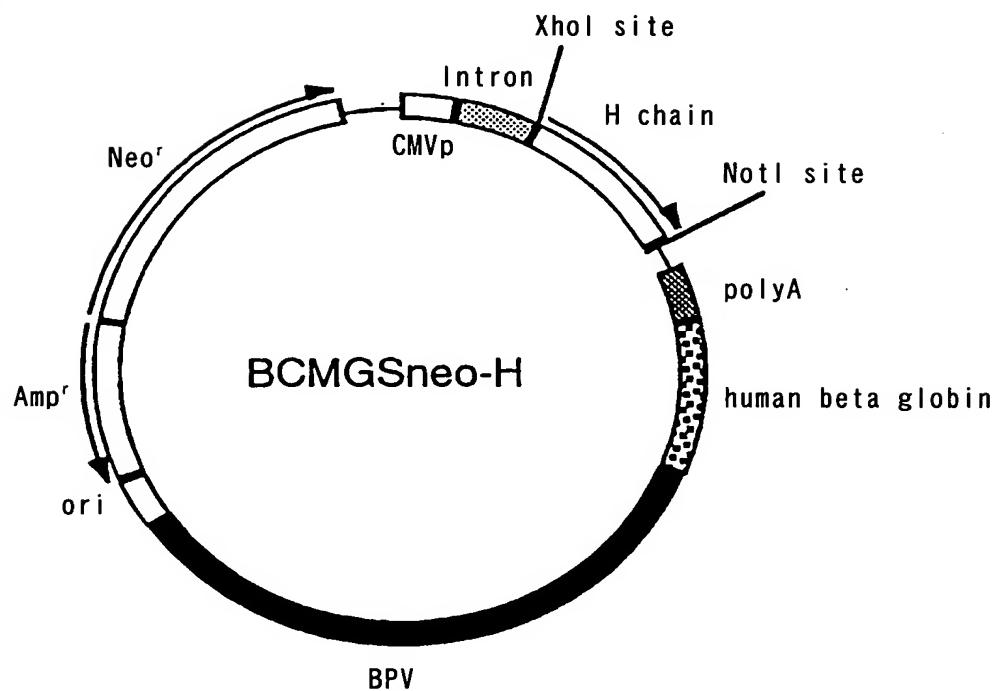
310 320 330 340 350 360
ACTGAGGATGATGCAATGTATTCTGTGCTCTATGGTACAGCACCCATTATGTTTCGGC
T E D D A M Y F C A L W Y S T H Y V F G

370 380
GGTGGAACCAAGGTCACTGTCCTAGGT
G G T K V T V L G

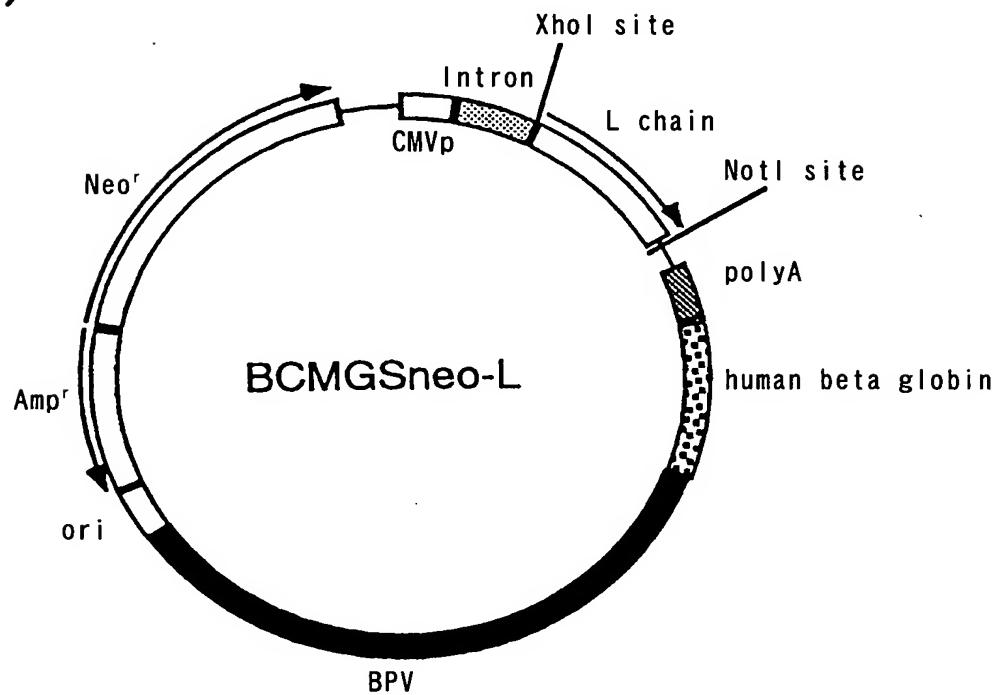
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Fig. 3

(A)



(B)



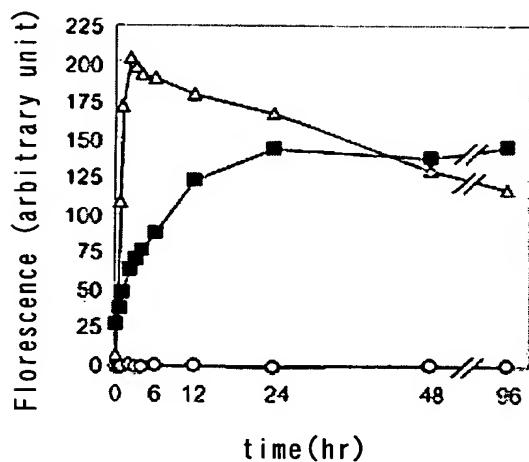
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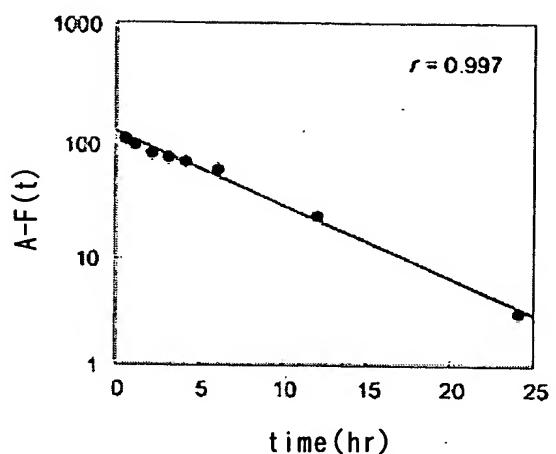
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Fig. 4

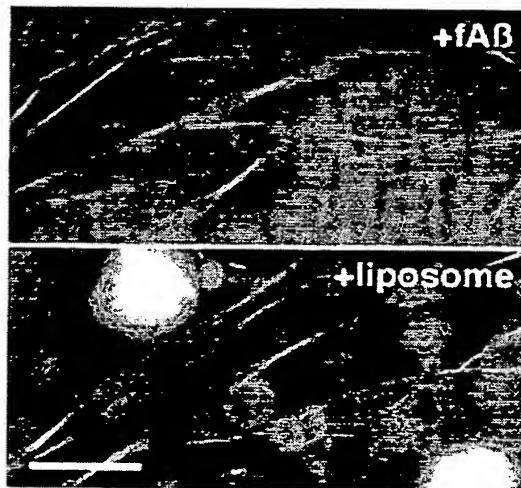
A



B



C



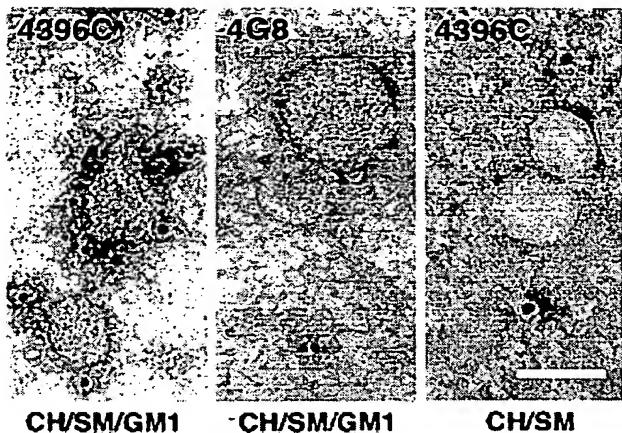
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Fig. 5

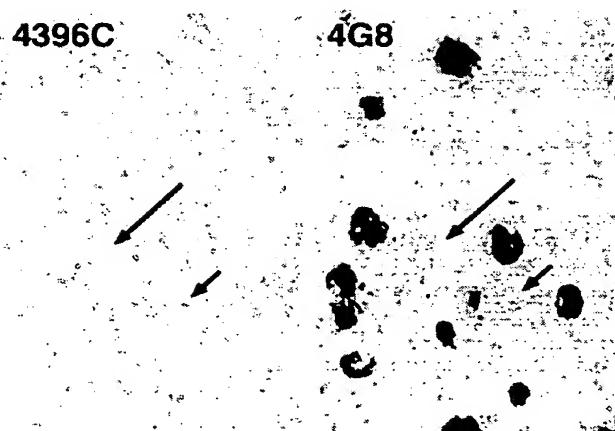
A



B



C



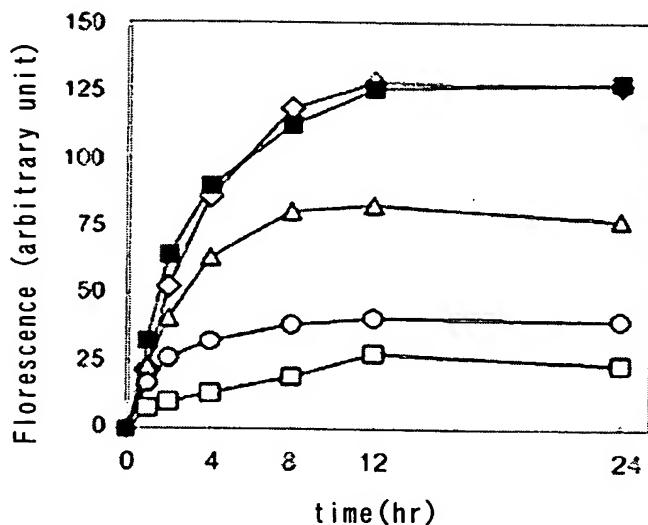
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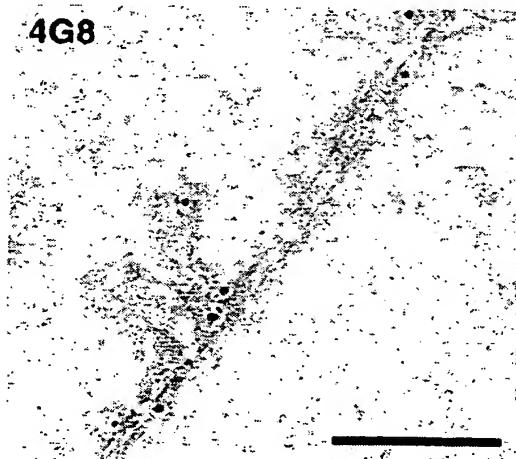
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Fig. 6

A



B



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Fig. 7

